

SEQUENCE LISTING



<110> Bayer Aktiengesellschaft

<120> Nucleic acids coding for new acetylcholine receptor beta subunits of insects

<130> Le A 34 147

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<150> DE 199 59 582.8

<151> 1999-12-10

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (43)..(1365)

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Met Thr Thr Thr
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ccc aag ata aag gca cca gtt tcc ggt cct gga ctg cca cta ctg ctg 102
Pro Lys Ile Lys Ala Pro Val Ser Gly Pro Gly Leu Pro Leu Leu Leu
5 10 15 20

caa atg cta atg ggg atg ctt ctt atg ggg ctg act tcc gtg cca ggc 150
Gln Met Leu Met Gly Met Leu Leu Met Gly Leu Thr Ser Val Pro Gly
25 30 35

gcc act gcc acc gcg gac ccc aag aac gcc aat gtc aag gcc ctg gat 198
Ala Thr Ala Thr Ala Asp Pro Lys Asn Ala Asn Val Lys Ala Leu Asp
40 45 50

cgc ctc cac gcc ggc ctg ttc acg aac tac gac agc gat gtg cag ccg 246
Arg Leu His Ala Gly Leu Phe Thr Asn Tyr Asp Ser Asp Val Gln Pro
55 60 65

gtg ttc caa gga acc ccc acg aac gtg tcc ctg gaa atg gtg gtc acc 294
Val Phe Gln Gly Thr Pro Thr Asn Val Ser Leu Glu Met Val Val Thr
70 75 80

tac ata gac atc gac gag ttg aac ggc aag ctg acc acc cac tgc tgg 342
Tyr Ile Asp Ile Asp Glu Leu Asn Gly Lys Leu Thr Thr His Cys Trp
85 90 95 100

ctg aat ctc cga tgg aga gac gag gag cgc gtg tgg caa ccg tca caa 390
Leu Asn Leu Arg Trp Arg Asp Glu Glu Arg Val Trp Gln Pro Ser Gln
105 110 115

tat	gac	aac	atc	acg	cag	atc	act	ttg	aag	tcc	agc	gag	gtc	tgg	acc	438
Tyr	Asp	Asn	Ile	Thr	Gln	Ile	Thr	Leu	Lys	Ser	Ser	Glu	Val	Trp	Thr	
			120					125					130			
ccc	caa	atc	aca	ctc	ttc	aac	ggc	gac	gaa	ggg	ggc	ctg	atg	gcc	gaa	486
Pro	Gln	Ile	Thr	Leu	Phe	Asn	Gly	Asp	Glu	Gly	Gly	Leu	Met	Ala	Glu	
		135					140					145				
acc	cag	gtg	acc	ctc	agc	cac	gat	ggc	cac	ttc	cgg	tgg	atg	cct	cca	534
Thr	Gln	Val	Thr	Leu	Ser	His	Asp	Gly	His	Phe	Arg	Trp	Met	Pro	Pro	
	150					155					160					
gcc	gtg	tac	acg	gcc	tac	tgc	gaa	ctc	aac	atg	ctc	aac	tgg	ccc	cac	582
Ala	Val	Tyr	Thr	Ala	Tyr	Cys	Glu	Leu	Asn	Met	Leu	Asn	Trp	Pro	His	
165					170					175					180	
gac	aag	cag	agc	tgc	aag	ttg	aag	atc	ggc	tcc	tgg	ggc	ctg	aag	gtc	630
Asp	Lys	Gln	Ser	Cys	Lys	Leu	Lys	Ile	Gly	Ser	Trp	Gly	Leu	Lys	Val	
			185						190					195		
gtc	ctg	ccg	gag	aac	ggc	acg	gcg	aga	gga	gag	tcc	ctt	gac	cac	gac	678
Val	Leu	Pro	Glu	Asn	Gly	Thr	Ala	Arg	Gly	Glu	Ser	Leu	Asp	His	Asp	
		200						205					210			
gac	ctg	gtt	cag	tca	ccg	gag	tgg	gaa	atc	gtg	gac	tcg	cga	gcc	cac	726
Asp	Leu	Val	Gln	Ser	Pro	Glu	Trp	Glu	Ile	Val	Asp	Ser	Arg	Ala	His	
	215					220					225					
ttt	gtc	agt	cag	gac	tac	tac	ggc	tac	atg	gag	tac	act	ctg	acg	gct	774
Phe	Val	Ser	Gln	Asp	Tyr	Tyr	Gly	Tyr	Met	Glu	Tyr	Thr	Leu	Thr	Ala	
	230					235					240					
cag	cgg	cgc	tcc	tcc	atg	tac	acg	gcc	gtc	atc	tac	aca	ccc	gcg	tcc	822
Gln	Arg	Arg	Ser	Ser	Met	Tyr	Thr	Ala	Val	Ile	Tyr	Thr	Pro	Ala	Ser	
245					250					255					260	
tgc	atc	gtc	atc	ctg	gcc	ctc	tca	gcc	ttc	tgg	ctg	cct	ccc	cac	atg	870
Cys	Ile	Val	Ile	Leu	Ala	Leu	Ser	Ala	Phe	Trp	Leu	Pro	Pro	His	Met	
			265					270						275		
ggc	ggc	gag	aag	atc	atg	atc	aac	ggc	ctg	ctc	atc	atc	gtg	atc	gcc	918
Gly	Gly	Glu	Lys	Ile	Met	Ile	Asn	Gly	Leu	Leu	Ile	Ile	Val	Ile	Ala	
		280						285					290			
gcc	ttc	ctc	atg	tac	ttc	gcc	cag	ctc	ctg	cca	gtg	ctg	tcc	aac	aat	966
Ala	Phe	Leu	Met	Tyr	Phe	Ala	Gln	Leu	Leu	Pro	Val	Leu	Ser	Asn	Asn	
		295					300				305					
act	cca	ctt	gtg	gta	atc	ttc	tac	agc	acc	agc	ctg	ctg	tat	ctg	agc	1014
Thr	Pro	Leu	Val	Val	Ile	Phe	Tyr	Ser	Thr	Ser	Leu	Leu	Tyr	Leu	Ser	
	310					315					320					
gtc	tcc	acc	atc	gtc	gag	gtt	cta	gtt	ctg	tac	ctg	gcc	aca	ggc	aag	1062
Val	Ser	Thr	Ile	Val	Glu	Val	Leu	Val	Leu	Tyr	Leu	Ala	Thr	Gly	Lys	
325					330				335						340	
cac	aag	agg	cgc	ctg	ccg	gag	gcg	ctg	aga	aag	ctg	ctg	cac	ggg	cac	1110
His	Lys	Arg	Arg	Leu	Pro	Glu	Ala	Leu	Arg	Lys	Leu	Leu	His	Gly	His	
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ctg ggc acg tgg ctg ctg ctc tcg gtg ttc agc acc act ggc gag tcg	1158
Leu Gly Thr Trp Leu Leu Leu Ser Val Phe Ser Thr Thr Gly Glu Ser	
360 365 370	
cag gcg gag aag acc aaa gag atg gac gag cac ccg tac gag gag gcg	1206
Gln Ala Glu Lys Thr Lys Glu Met Asp Glu His Pro Tyr Glu Glu Ala	
375 380 385	
gac gag cag gag tcc agt ccg ctg ggc atc aac cac acc gag gtg ccg	1254
Asp Glu Gln Glu Ser Ser Pro Leu Gly Ile Asn His Thr Glu Val Pro	
390 395 400	
ggc gcc aag gcc aac cag ttc gac tgg gcg ctg ctg gcc acc gcc gtg	1302
Gly Ala Lys Ala Asn Gln Phe Asp Trp Ala Leu Leu Ala Thr Ala Val	
405 410 415 420	
gac cgc att tcc ttc gtt tcc ttc agc ctg gcc ttc ctc att ctg gcc	1350
Asp Arg Ile Ser Phe Val Ser Phe Ser Leu Ala Phe Leu Ile Leu Ala	
425 430 435	
atc agg tgc tcc gtg tagggatgct cgagactcaa ggccacatcc caagccagtg	1405
Ile Arg Cys Ser Val	
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cgcaactctga actagttttg catttgcgat ttcattgtatt taatgtgtgt gcgaacttat	1465
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Ser Val Pro Gly Ala Thr Ala Thr Ala Asp Pro Lys Asn Ala Asn Val	
35 40 45	
Lys Ala Leu Asp Arg Leu His Ala Gly Leu Phe Thr Asn Tyr Asp Ser	
50 55 60	
Asp Val Gln Pro Val Phe Gln Gly Thr Pro Thr Asn Val Ser Leu Glu	
65 70 75 80	
Met Val Val Thr Tyr Ile Asp Ile Asp Glu Leu Asn Gly Lys Leu Thr	
85 90 95	
Thr His Cys Trp Leu Asn Leu Arg Trp Arg Asp Glu Glu Arg Val Trp	
100 105 110	
Gln Pro Ser Gln Tyr Asp Asn Ile Thr Gln Ile Thr Leu Lys Ser Ser	
115 120 125	

Glu Val Trp Thr Pro Gln Ile Thr Leu Phe Asn Gly Asp Glu Gly Gly
 130 135 140
 Leu Met Ala Glu Thr Gln Val Thr Leu Ser His Asp Gly His Phe Arg
 145 150 155 160
 Trp Met Pro Pro Ala Val Tyr Thr Ala Tyr Cys Glu Leu Asn Met Leu
 165 170 175
 Asn Trp Pro His Asp Lys Gln Ser Cys Lys Leu Lys Ile Gly Ser Trp
 180 185 190
 Gly Leu Lys Val Val Leu Pro Glu Asn Gly Thr Ala Arg Gly Glu Ser
 195 200 205
 Leu Asp His Asp Asp Leu Val Gln Ser Pro Glu Trp Glu Ile Val Asp
 210 215 220
 Ser Arg Ala His Phe Val Ser Gln Asp Tyr Tyr Gly Tyr Met Glu Tyr
 225 230 235 240
 Thr Leu Thr Ala Gln Arg Arg Ser Ser Met Tyr Thr Ala Val Ile Tyr
 245 250 255
 Thr Pro Ala Ser Cys Ile Val Ile Leu Ala Leu Ser Ala Phe Trp Leu
 260 265 270
 Pro Pro His Met Gly Gly Glu Lys Ile Met Ile Asn Gly Leu Leu Ile
 275 280 285
 Ile Val Ile Ala Ala Phe Leu Met Tyr Phe Ala Gln Leu Leu Pro Val
 290 295 300
 Leu Ser Asn Asn Thr Pro Leu Val Val Ile Phe Tyr Ser Thr Ser Leu
 305 310 315 320
 Leu Tyr Leu Ser Val Ser Thr Ile Val Glu Val Leu Val Leu Tyr Leu
 325 330 335
 Ala Thr Gly Lys His Lys Arg Arg Leu Pro Glu Ala Leu Arg Lys Leu
 340 345 350
 Leu His Gly His Leu Gly Thr Trp Leu Leu Leu Ser Val Phe Ser Thr
 355 360 365
 Thr Gly Glu Ser Gln Ala Glu Lys Thr Lys Glu Met Asp Glu His Pro
 370 375 380
 Tyr Glu Glu Ala Asp Glu Gln Glu Ser Ser Pro Leu Gly Ile Asn His
 385 390 395 400
 Thr Glu Val Pro Gly Ala Lys Ala Asn Gln Phe Asp Trp Ala Leu Leu
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21